

1 CGGCACGAGGGCATGGGGCGGCTGGTTCGTGCTGGGAGCTGCCGTCTTTCTGCTGGGA 60  
 1 M G R L V L L W G A A V F L L G 16

61 GGCTGGATGGCTTTGGGGCAAGGAGGACGACAGAGAAGGATACAGATTACATCTAC 120  
 17 G W M A L G Q G G A A E G V Q I Q I I Y 36

121 TTCAATTAGAAACCGTGCAGGTGACATGGAAATGCCAGCAAACTCTCAGGACCAACCTG 180  
 37 F N L E T V Q V T W N A S K Y S R T N L 56

181 ACTTTCCACTACAGATTCAACCGTGATGAGGCGCTATGACAGTGCACCAACTACCTTCTC 240  
 57 T F H Y R F N G D E A Y D Q C T N Y L L 76

241 CAGGAAGGTCACTTCGGGGTGCTCTCTAGACGCAGAGCAGAGACGACATCTCTAT 300  
 77 Q E G H T S G C L L D A E Q R D D I L Y 96

301 TTCTCCATCAGGAATGGGACGCACCCCGTTTTCACCGCAAGTCGCTGGATGGTTTATTC 360  
 97 F S I R N G T H P V F T A S R W M V Y Y 116

361 CTGAACCCAGTTCCCGAAGCACGTGAGATTTCGTGGCATCAGGATCGAGTGCAGGTG 420  
 117 L K P S S P K H V R F S W H Q D A V T V 136

421 ACGTGTCTGACCTGTCTACGGGATCCTCTATGAGGTTCAGTACCGGAGCCCTTC 480  
 137 T C S D L S Y G D L L Y E V Q Y R S P F 156

481 GACACCGAGTGGCAGTCCAAACAGGAAATACCTGCAAGTCCACATAGAAGGCTTGGAT 540  
 157 D T E W Q S K Q E N T C N V T I E G L D 176

541 GCGGAGAAGTGTTACTCTTTCTGGGTGAGGTGAAGGCTATGGAGGATATATGGGCA 600  
 177 A E K C Y S F W V R V K A M E D V Y G P 196

601 GACACATACCAAGCGACTGGTCAGAGGTGACATGCTGGCAGAGAGGCGAGATTCCGGAT 660  
 197 D T Y P S D W S E V T C W Q R G E I R D 216

661 GCGTGTGAGAGACACCAAGCGCTCCCAACCAAGCTGTCCAAATTATTTTAAATTTC 720  
 217 A C A E T P T P P K P K L S K F I L I S 236

721 AGCGTGGGCATCCTTCTGATGGTGTCTCTCCTCCTTCTGTCTTTATGGAATATATGAGA 780  
 237 S L A I L L M V S L L L S L W K L W R 256

781 GTGAAGAAGTTTCTCATTCAGCGGTGCCAGACCCGAAATTCATCTTCCCGGGCTCTTT 840  
 257 V K K F L I P S V P D P K S I F P G L F 276

841 GAGATACACCAAGGAACTTCCAGGAGTGGATCAGACACCCAGAACGTTGGCCACCTC 900  
 277 E I H Q G N F Q E W I T D T Q N V A H L 296

FIG. 1A

09376430-081809

901 CACAAGATGGCAGGTGCAGAGCAAGAAAGTGGCCCCGAGGAGCCCCCTGGTAGTCCAGTTG 960  
 297 H K M A G A E Q E S G P E E P L V V Q L 316

961 GCCAAGACTGAAGCCGAGTCTCCAGGATGCTGGACCCACAGACCGAGGAGAAAGAGGCC 1020  
 317 A K T E A E S P R M L D P Q T E E K E A 336

1021 TCTGGGGGATCCCTCCAGCTTCCCCACCAGCCCCCTCCAAGCGGATGTGGTCACAATC 1080  
 337 S G G S L Q L P H Q P L Q G G D V V T I 356

1081 GGGGGCTTACCTTTGTGATGAATGACCGCTCTACGTGGCGTTGTGATGGACACACCAC 1140  
 357 G G F T F V M N D R S Y V A L \* 372

1141 TGTCAAAGTCAACGTCAGGATCCACGTTGACATTTAAAGACAGAGGGGACTGTCCCGGG 1200

1201 ACTCCACACCACCATGGATGGGAAGTCTCCAGCCCAATGATGGTAGGACTAGGAGACTCT 1260

1261 GAAGACCCAGCCTCACCGCCTAATGGGCGCACTGCCTGTACTTTCCCCCACATGAGT 1320

1321 CTCTGTGTCAAAGGCTTGATGGCAGATGGGAGCCAAATGTCTCCAGGAGATTTACTCCA 1380

1381 GTTCCTTTTCGTGCTGAACGTTGTACATAAACCACAGGCAGCACTCCAAAATGCTG 1440

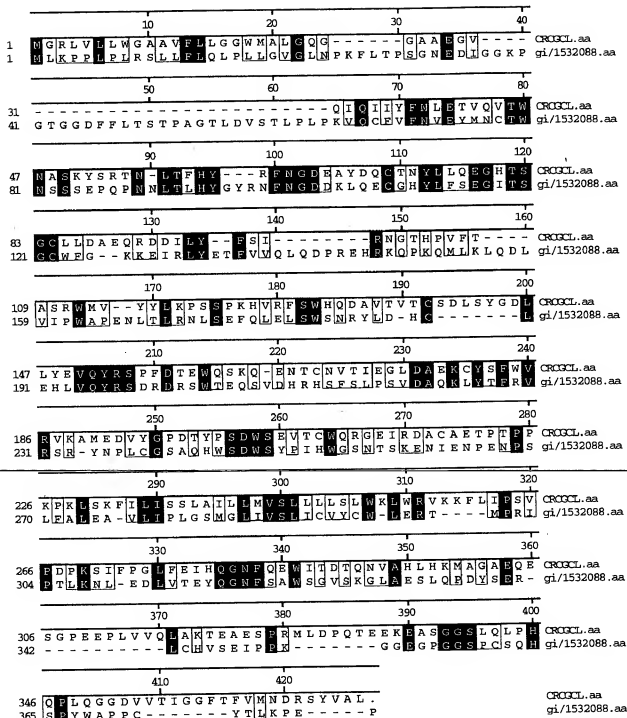
1441 TAAAACCATCTTCCCACTCTGTGAGTCCCCAGTCCCGTCCATGTACCTGTTCATAGCAT 1500

1501 TGGATTCTCGGAGGATTTTGTGTCTGTTTGAGACTCCAAACCACTCTACCCCTACAAA 1560

1561 AAAAAAAAAAAAAA 1573

09376430.081899

FIG. 1B



Decoration 'Decoration #1': Box residues that match the consensus named 'Consensus #2' exactly.

Decoration 'Decoration #2': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

FIG. 2

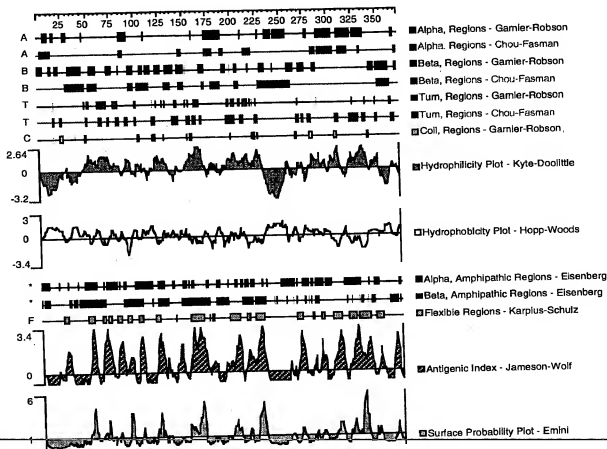


FIG. 3

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